

P17.026.A A Flexible and Shared Information Fine-mapping Approach with an application to 33 cardiometabolic traits from a Ugandan cohort

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Joint fine-mapping that leverages information between related quantitative traits could improve accuracy and precision over single-trait fine-mapping. Using summary statistics, flashfm (FLexible And SHared information Fine-Mapping) fine-maps association signals for multiple traits measured in the same sample, borrowing information between them in a Bayesian framework. In addition, we address key challenges that arise in real data: missing trait measurements and related individuals. Simulation studies of two traits measured in a single cohort with varying sample size, varying trait correlation, and varying proportion of missing data from one trait demonstrate that flashfm reduces the set of potential causal variants by 30% compared to single-trait fine-mapping when traits share a causal variant; when there are no shared causal variants flashfm has similar results to single-trait fine-mapping. In fine-mapping signals from 33 cardiometabolic traits in a Ugandan cohort, flashfm resulted in an average SNP group size reduction of 29% in 34% of the regions that had signals for at least two traits, compared to single-trait fine-mapping. Flashfm is able to make use of previously generated single-trait fine-mapping results and is freely available as an R package (<https://github.com/jennasimit/flashfm>). It is computationally efficient and increases fine-mapping accuracy and resolution at lower cost, and is more feasible than collecting larger samples.

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